Please find below and/or attached an Office communication concerning this application or proceeding.

Commissioner of Patents and Trademarks

SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.

EXAMINER

ART UNIT	PAPER NUMBER
	9

DATE MAILED:

Please find below a communication from the EXAMINER in charge of this application.

Commissioner of Patents

Serial No. 09/312,596

1.   The reply filed 3 November 2000 (Paper No. 9) is not fully responsive to the communication mailed 28 May 1999 (Paper No. 3) for the reason(s) set forth on the attached Notice To Comply With The Sequence Rules or CRF Diskette Problem Report.

Since the above-mentioned reply appears to be *bona fide*, applicant is given a TIME PERIOD of **ONE (1) MONTH** or **THIRTY (30) DAYS**, from the mailing date of this notice, whichever is longer, within which to supply the omission or correction in order to avoid abandonment. EXTENSIONS OF THIS TIME LIMIT MAY BE GRANTED UNDER 37 CFR 1.136(a).

2.   Any inquiry concerning this communication or earlier communications from the examiner should be directed to Michael Pak, whose telephone number is (703) 305-7038. The examiner can normally be reached on Monday through Friday from 5:50 AM to 2:20 PM.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Yvonne Eyler, can be reached on (703) 308-6564.

Official papers filed by fax should be directed to (703) 308-4242. Faxed draft or informal communications with the examiner should be directed to (703) 308-0294.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the Group receptionist whose telephone number is (703) 308-0196.

Michael D. Pak

Michael Pak
Primary Patent Examiner
Art Unit 1646
18 December 2000

SUBSTITUTE PTOL-90

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

☐ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.

☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

☐ 7. Other:

Applicant Must Provide:

☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".

☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
For PatentIn software help, call (703) 308-6856

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE

ERROR DETECTED **SUGGESTED CORRECTION** SERIAL NUMBER: _09/312,596_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

RECEIVED

NOV 29 2000

TECH CENTER 1600/2900

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>**
sections for Artificial or Unknown sequences.

8 _____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 ✓ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism (NEW RULES)
Sequence(s) _____ are missing this mandatory field or its response.

12 _____ Use of <220>Feature (NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

AKS-Biotechnology Systems Branch- 5/15/99

1646

```
RAW SEQUENCE LISTING            DATE: 11/20/2000
PATENT APPLICATION:  US/09/312,596   TIME: 08:38:37

Input Set : A:\593601.app
Output Set: N:\CRF3\11202000\I312596.raw

3  <110> APPLICANT: Role, Lorna W.
4        Talmage, David
5        Bao, Jianxin
7  <120> TITLE OF INVENTION: A-FORM OF CYTOPLASMIC DOMAIN OF nARIA (CRD-NEUREGULIN
8        AND USES THEREOF
10 <140> FILE REFERENCE: 0575/59360
12 <140> CURRENT APPLICATION NUMBER: 09/312,596
13 <111> CURRENT FILING DATE: 1999-05-14
15 <160> NUMBER OF SEQ ID NOS: 4
17 <170> SOFTWARE: PatentIn Ver. 2.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 3212
21 <212> TYPE: DNA
22 <213> ORGANISM: CHICKEN nARIA
24 <400> SEQUENCE: 1
25 cggatgctgc tgctactgtc actctgccg ctgccgctgt tgttacagat tttgcttttg 60
26 ctccttctac cgcatgacaa ttgtttcct cgcctaagca gataccaacc tcagatgctc 120
27 aaggtgagag tcttgccttt cgctctggc tattcgttca cttaatccgg tcaattgtt 180
28 cgctgctcgt ggttgtcttt ctccccgcc tcctccccc tgttttgttt tgtttcgctt 240
29 gctttcgggg agacggtcct tccctcagtc agaagagctg gaattgcttg agagcgtat 300
30 aaggaattat aaaagtggca agaaaacacg agcgcagtga ctacagagct accctcggct 360
31 tcggcaaggc agcttgagcg acaagaggct cggcgcaggg gcgaggggtc tccttttcc 420
32 cgtgcgttcc tcttctccca gttcggatga tgttgctgtt tcggacctct cgctgactcc 480
33 tgccctgtga ttttgctga gcgctgtgac tgttactccg tctcttctg tctgtgtttc 540
34 acagtgatgg actgtgatag agttaaggcc tttgaggt gagctgtgtc acagctaatg 600
35 cttaaacatg tctgaagtag gcaccgacac ttccccaac ccctcaagctc agctgagccc 660
36 tgatgcatcc cttggcggac tccggcctga ggagaacatg ccggggcccc acagagagga 720
37 cagcaggggtc ccagttgttgg cagcctggc ctcgacctgc tgcgtgtgcc tggaagcaga 780
38 ucgactgaag ggctgctcca actctgagaa aatctgcatc gccctatcc tagcttgcct 840
39 actcaagcctc tgcctctgca ttgctggcct caagtgggtc tttatgaaca agatttttga 900
40 gtatgactct cctacacacc ttgacctgg gaggataggg caagaccaaa ggagcactgt 960
41 ggatcctaca gctctgtctg cctggtgcc ttcggaggtg tatgcctcac ccttcccat 1020
42 acctagcctt gagagcaagg ctgaagtgac agtgcaaact gacagctgc tcgtgcctc 1080
43 caggccctc cttcagcctt ctctctacaa ccgcatccta gatctcgggt tgtggtcctc 1110
44 tgccacacg tcactgtcac catcctcct ggagcctacc acggcatctc aggcacaagc 1200
45 aacagaaacc aatctccaaa ctgctccaaa actccact tctacatcta caactggac 1260
46 aagtcatctc acaaatgtg acataaagca gaaagccttc tgtgtaaatg gggagagtg 1320
47 ctacatggta aaagacctcc caaacccc acgatacct tgcaggtcc caatgaatt 1380
48 tactggtgat cgctgccaaa actacgtaat ggccagcttc tacaagcatc ttgggattga 1410
49 atttatggaa gctgaggaac tgtaccagaa acggtgctg accataactg gcatttgcat 1500
50 tgctcttcta gtagttggca tcatgtgtat ggtggctac tgcaaaacca agaagcagag 1560
51 gaaaaagttg catgaccgcc ttcggcagag ccttgctca gagaggaaca acgttatgaa 1620
52 catggcaaat gggccacacc accccaacc accaccagac aatgtccagc tggtgaatca 1680
53 gtacgtttca aaaaacataa tctccagtga acgtgtcgtt gagcgagaaa ccagacctc 1740
54 gtttccaca agccactaca cctcaacaac tcatcactcc atgacagtca cccagacgcc 1800
55 taaccacagc tggagtaaty gccataccga aagcattctc tccgaaagcc actccgtgct 1860
56 cgtcagctcc tcagtggaga atagcaggca caccagccca acagggccac gaggccgcct 1920
```

```
RAW SEQUENCE LISTING                    DATE: 11/20/2000
PATENT APPLICATION:  US/09/312,596      TIME: 08:38:37

Input Set : A:\593601.app
Output Set: N:\CRF3\11202000\I312596.raw

57 caatggcatt ggtgggcaa gggaggcaa cagcttcctc cggcatgcaa gagagacccc 1980
58 tgactcctac cgagactctc ctcacagtga aaggtatgtc tcagctatga ccacaccagc 2040
59 tcgcatgtca cccgttgatt tccacactcc aacttctccc aagtcccctc catctgaaat 2100
60 gtcaccacca gtttccaget tgaccatctc catccttcg gtggcggtga gtcccttat 2160
61 ggacgaggag agaccgctgc tattggtgac cccaccacgg ctgcgtgaga agtacgacaa 2220
62 ccacettcag caattcaact ccttccacaa caatcccacc catgagagca acagtctgcc 2280
63 acccagtcct ctgaggatag tggaggatga agggtatgag accacgcagg agtacgaacc 2340
64 agcacaggag cctccaaaga aactcaccaa cagccggagg gtgaaaagaa caaagcccaa 2400
65 tggccatatt tccagcaggg tagaagtgga ctccgacaca agctctcaga gcactagctc 2460
66 tgagagcgaa acagaagatg aaagaatagg tgaggataca ccatttctta gcatacaaaa 2520
67 tcccatggca accagtctgg agccagccgc tgcatatcgg ctggctgaga acaggactaa 2580
68 cccagcaaat cgcttctcca caccagaaga gttgcaagca aggttgtcca gtgtaatagc 2640
69 taaccaagac cctattgctg tataagacat aaacaaaaca catagattca catgtaaaac 2700
70 tttatrttat ataatgaagt attccacctt taaattaaac aatttatttt attrtagcaa 2760
71 ttccgctgat agaaaacaag agtggaaaaa gaaactttta taaattaagt atacgtatgt 2820
72 acaaatgtgt tatgtgccat atgtagcaat tttttacagt atttccaaaa tgggqaaaga 2880
73 tatcaatggt gcctttatgt tatgttatgt tgagagcaag tttttgtacag ctacaatgat 2940
74 tgctgtcccg tagtattttg caaaaccttc tagccctcag ttgttctggc tttttttgtgc 3000
75 attgcattat aatgactgga tgtatgattt gcaaaaattg cagaagtccc cattttgcttg 3060
76 ttgtgggaatc cccagatcaa aaagccctat tatggcactc acaccctatc cacttcacca 3120
77 ggaaaaaaaa aaaatcaaaa aaaaaaaaaa aaaaaaaaga aaagaaagag aaaaaagaaa 3180
78 agaaaaagaa aaaaaaagct gaaaaaataa aa                                 3212
81 <210> SEQ ID NO: 2
82 <211> LENGTH: 1070
83 <212> TYPE: PRT
84 <213> ORGANISM: CHICKEN GARIA
86 <400> SEQUENCE: 2
87 Gly Cys Cys Cys Tyr Cys His Phe Cys Arg Cys Arg Cys Cys Tyr Arg
88  1               5               10               15
```

W--> 90 Phe Cys Phe Cys Ser Phe Tyr Arg Met Thr Ile Val Phe Leu Ala (Xaa)
```
91               20               25               30
```

W--> 93 Ala Asp Thr Ser Leu Arg Cys Ser Arg (Xaa) Glu Ser Cys Leu Ser Leu
```
94       35               40               45
96 Trp Ala Ile Gly Ser Leu Asn Pro Val Asn Leu Phe Ala Ala Arg Gly
97       50               55               60
99 Cys Leu Ser Pro Arg Pro Pro Ser Pro Cys Phe Val Leu Phe Arg Leu
100  65               70               75               80
102 Leu Ser Gly Gly Arg Ser Phe Pro Gln Ser Glu Glu Leu Glu Leu Leu
103               85               90               95
105 Glu Arg Arg Ile Arg Asn Tyr Lys Ser Gly Gln Glu Thr Arg Ala Gln
106               100               105               110
```

W--> 108 (Xaa) Leu Gln Ser Cys Pro Trp Leu Arg Gln Gly Ser Val Ser Gly Arg
```
109       115               120               125
111 Gly Leu Gly Gln Gly Ala Gly Gly Leu Leu Phe Pro Val Arg Ser Ser
112       130               135               140
114 Ser Pro Ser Ser Asp Asp Val Ala Val Ser Asp Leu Ser Leu Thr Pro
115 145               150               155               160
```

W--> 117 Ala Leu (Xaa) Phe Leu Leu Ser Ala Val Thr Val Thr Pro Ser Leu Ser
```
118               165               170               175
```

[Handwritten note:] missing mandatory <220> to <223> features to explain "Xaa's" in the sequence. See # 10 on the Error Summary Sheet.

refer to p.2

```
W--> 120 Val Cys Val Ser Gln Xaa Trp Thr Val Ile Glu Leu Arg Pro Phe Gly
     121         180                 185                 190
W--> 123 Gly Glu Leu Cys His Ser Xaa Cys Leu Asn Met Ser Glu Val Gly Thr
     124         195                 200                 205
     126 Glu Thr Phe Pro Ser Pro Ser Ala Gln Leu Ser Pro Asp Ala Ser Leu
     127         210                 215                 220
     129 Gly Gly Leu Pro Ala Glu Glu Asn Met Pro Gly Pro His Arg Glu Asp
     130 225                 230                 235                 240
     132 Ser Arg Val Pro Gly Val Ala Gly Leu Ala Ser Thr Cys Cys Val Cys
     133                 245                 250                 255
     135 Leu Glu Ala Glu Arg Leu Lys Gly Cys Leu Asn Ser Glu Lys Ile Cys
     136             260                 265                 270
     138 Ile Ala Pro Ile Leu Ala Cys Leu Leu Ser Leu Cys Leu Cys Ile Ala
     139         275                 280                 285
     141 Gly Leu Lys Trp Val Phe Val Asp Lys Ile Phe Glu Tyr Asp Ser Pro
     142         290                 295                 300
     144 Thr His Leu Asp Pro Gly Arg Ile Gly Gln Asp Pro Arg Ser Thr Val
     145 305                 310                 315                 320
     147 Asp Pro Thr Ala Leu Ser Ala Trp Val Pro Ser Glu Val Tyr Ala Ser
     148                 325                 330                 335
     150 Pro Phe Pro Ile Pro Ser Leu Glu Ser Lys Ala Glu Val Thr Val Gln
     151             340                 345                 350
     153 Thr Asp Ser Ser Leu Val Pro Ser Arg Pro Phe Leu Gln Pro Ser Leu
     154             355                 360                 365
     156 Tyr Asn Arg Ile Leu Asp Val Gly Leu Trp Ser Ser Ala Thr Pro Ser
     157     370                 375                 380
     159 Leu Ser Pro Ser Ser Leu Glu Pro Thr Thr Ala Ser Glu Ala Gln Ala
     160 385                 390                 395                 400
     162 Thr Glu Thr Asn Leu Gln Thr Ala Pro Lys Leu Ser Thr Ser Thr Ser
     163                 405                 410                 415
     165 Thr Thr Gly Thr Ser His Leu Thr Lys Cys Asp Ile Lys Gln Lys Ala
     166             420                 425                 430
     168 Phe Cys Val Asn Gly Gly Glu Cys Tyr Met Val Lys Asp Leu Pro Asn
     169         435                 440                 445
     171 Pro Pro Arg Tyr Leu Cys Arg Cys Pro Asn Glu Phe Thr Gly Asp Arg
     172     450                 455                 460
     174 Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Lys His Leu Gly Ile Glu
     175 465                 470                 475                 480
     177 Phe Met Glu Ala Glu Glu Leu Tyr Gln Lys Arg Val Leu Thr Ile Thr
     178             485                 490                 495
     180 Gly Ile Cys Ile Ala Leu Leu Val Val Gly Ile Met Cys Val Val Ala
     181         500                 505                 510
     183 Tyr Cys Lys Thr Lys Lys Gln Arg Lys Lys Leu His Asp Arg Leu Arg
     184         515                 520                 525
     186 Gln Ser Leu Arg Ser Glu Arg Asn Asn Val Met Asn Met Ala Asn Gln
     187     530                 535                 540
     189 Pro His His Pro Asn Pro Pro Pro Asp Asn Val Gln Leu Val Asn Gln
     190 545                 550                 555                 560
     192 Tyr Val Ser Lys Asn Ile Ile Ser Ser Glu Arg Val Val Glu Arg Glu
```

RAW SEQUENCE LISTING   DATE: 11/20/2000
PATENT APPLICATION: US/09/312,596 TIME: 08:38:37

Input Set : A:\593601.app
Output Set: N:\CRF3\11202000\I312596.raw

```
193                    565                570                575
195 Thr Glu Thr Ser Phe Ser Thr Ser His Tyr Thr Ser Thr Thr His His
196              580                585                590
198 Ser Met Thr Val Thr Gln Thr Pro Ser His Ser Trp Ser Asn Gly His
199          595                600                605
201 Thr Glu Ser Ile Leu Ser Glu Ser His Ser Val Leu Val Ser Ser Ser
202      610                615                620
204 Val Glu Asn Ser Arg His Thr Ser Pro Thr Gly Pro Arg Gly Arg Leu
205 625              630                635                640
207 Asn Gly Ile Gly Gly Pro Arg Glu Gly Asn Ser Phe Leu Arg His Ala
208              645                650                655
210 Arg Glu Thr Pro Asp Ser Tyr Arg Asp Ser Pro His Ser Glu Arg Tyr
211          660                665                670
213 Val Ser Ala Met Thr Thr Pro Ala Arg Met Ser Pro Val Asp Phe His
214          675                680                685
216 Thr Pro Thr Ser Pro Lys Ser Pro Pro Ser Glu Met Ser Pro Pro Val
217      690                695                700
219 Ser Ser Leu Thr Ile Ser Ile Pro Ser Val Ala Val Ser Pro Phe Met
220 705              710                715                720
222 Asp Glu Glu Arg Pro Leu Leu Leu Val Thr Pro Pro Arg Leu Arg Glu
223          725                730                735
225 Lys Tyr Asp Asn His Leu Gln Gln Phe Asn Ser Phe His Asn Asn Pro
226          740                745                750
228 Thr His Glu Ser Asn Ser Leu Pro Pro Ser Pro Leu Arg Ile Val Glu
229          755                760                765
231 Asp Glu Glu Tyr Glu Thr Thr Gln Glu Tyr Glu Pro Ala Gln Glu Pro
232      770                775                780
234 Pro Lys Lys Leu Thr Asn Ser Arg Arg Val Lys Arg Thr Lys Pro Asn
235 785              790                795                800
237 Gly His Ile Ser Ser Arg Val Glu Val Asp Ser Asp Thr Ser Ser Gln
238              805                810                815
240 Ser Thr Ser Ser Glu Ser Glu Thr Glu Asp Glu Arg Ile Gly Glu Asp
241          820                825                830
243 Thr Pro Phe Leu Ser Ile Gln Asn Pro Met Ala Thr Ser Leu Glu Pro
244          835                840                845
246 Ala Ala Ala Tyr Arg Leu Ala Glu Asn Arg Thr Asn Pro Ala Asn Arg
247      850                855                860
249 Phe Ser Thr Pro Glu Glu Leu Gln Ala Arg Leu Ser Ser Val Ile Ala
250 865              870                875                880
W--> 252 Asn Gln Asp Pro Ile Ala Val (Xaa) Asp Ile Asn Lys Thr His Arg Phe
253              885                890                895
255 Thr Cys Lys Thr Leu Phe Tyr Ile Met Lys Tyr Ser Thr Phe Lys Leu
256          900                905                910
258 Asn Asn Leu Phe Tyr Phe Ser Asn Ser Ala Asp Arg Lys Gln Glu Trp
259          915                920                925
W--> 261 Lys Lys Lys Leu Leu (Xaa) Ile Lys Tyr Thr Tyr Val Gln Met Cys Tyr
262      930                935                940
264 Val Pro Tyr Val Ala Ile Phe Tyr Ser Ile Ser Lys Met Gly Lys Asp
265 945              950                955                960
```

refer to p. 2

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/312,596

DATE: 11/20/2000
TIME: 08:38:38

Input Set : A:\593601.app
Output Set: N:\CRF3\11202000\I312596.raw

```
      267 Ile Asn Gly Ala Phe Met Leu Cys Tyr Val Glu Ser Lys Phe Cys Thr
      268               965                   970                   975
W-->  270 Ala Thr Met Ile Ala Val Pro Xaa Tyr Phe Ala Lys Pro Ser Ser Pro
      271               980                   985                   990
      273 Gln Leu Phe Trp Leu Phe Cys Ala Leu His Tyr Asn Asp Trp Met Tyr
      274               995                  1000                  1005
      276 Asp Leu Gln Glu Leu Gln Lys Ser Pro Phe Ala Cys Cys Gly Ile Pro
      277      1010                  1015                  1020
      279 Arg Ser Lys Ser Pro Val Met Ala Leu Thr Pro Tyr Pro Leu His Gln
      280 1025                  1030                  1035                  1040
      282 Glu Lys Lys Lys Ile Lys Lys Lys Lys Lys Lys Arg Lys Glu Arg
      283               1045                  1050                  1055
W-->  285 Glu Lys Arg Lys Glu Lys Glu Lys Lys Ser Xaa Lys Asn Lys
      286               1060                  1065                  1070
      289 <210> SEQ ID NO: 3
      290 <211> LENGTH: 1351
      291 <212> TYPE: DNA
      292 <213> ORGANISM: HUMAN DARIA
      294 <400> SEQUENCE: 3
      295 cggcctataa gatgctgtat catttggttg ggggggcctc tacgtggtaa tggaccgtaa 60
      296 gagcggccag gccttcttct ggaggtgagc cgatggagat ttattcccca gacatgtctg 120
      297 aggtcgccac cgagagggtcc tccagcccct ccactcagct gagtgcagac ccatctcttg 180
      298 atgggcttcc ggcagcagaa gacatgccag agcccagac tgaagatggg agaacccctg 240
      299 gactcgtggg cctggccgtg ccctgctgtg cgtgcctaga agctgagcac ctgagaggtt 300
      300 gcctcaactc agagaaaatc tgcattgtcc ccatcctgac ttgcctggtc agcctctgcc 360
      301 tctgcatcgc cggcctcaag tgggtatttg tggacaagat cttgaatat gactctccta 420
      302 ctcaccttaa ccctggggg traggccagg acccatttat ttctctggac gcaactgctg 480
      303 cctcagctgt gtgggtgtcg tctgaggcat acacttcacc tgtctctagg gctcaatctg 540
      304 aaagtgaggt tcaagttaca gtgcaaggtg acaaggctgt tgtctccttt gaaccatcag 600
      305 cggcacgac acgaagaat cgtattttg cctttctt ctgcgtcc actgcgccat 660
      306 ccttccttc acccacccgg aacctgagg tgaacacgcc caagtcagca actcagccac 720
      307 aaacaacaga aactaatctc caaactgctc ctaaactttc tacatctaca tccaccactg 780
      308 ggacaagca tctttaaaa tgtgcggaga aggagaaaac tttctgtatg aatggaggg 840
      309 agtgcttcat ggttaaagac ctttcaaacc cctcgagata cttgtcaaa ggcggaggag 900
      310 ctgtaccaga agagagtgct gaccataacc ggcatctaca tcgcctcct tgtggtcggc 960
      311 atcatgtgtg tggtggccta ctgcaaaacc aagaaatcagc ggaaaaaget gcatgacgt 1020
      312 cttcagcaga gccttcggtc tgaacagaac aatacgatga acattaccaa tgggcctcac 1080
      313 catcctcacc caccccccga gaatgtccag ctggtgaatc aatacgtatc taaaaargtc 1140
      314 atctccagtg agcatattgr tgagagagaa gcagagacat cctttccac cagtcactat 1200
      315 acttccacag cccatcactc cactactgtc acccagactc ctagccacag ctggagcaac 1260
      316 ggacacactg aaaagcatcct ttccgaaagc cactctgtaa tcgtgatgtc atccgtagaa 1320
      317 aacagtaggc acagcagccc aactgggcc g 1351
      320 <210> SEQ ID NO: 4
      321 <211> LENGTH: 448
      322 <212> TYPE: PRT
      323 <213> ORGANISM: HUMAN DARIA
      325 <400> SEQUENCE: 4
W-->  326 Ala Cys Lys Met Leu Tyr His Leu Val Gly Gly Ala Ser Ala Trp Xaa
      327   1                 5                  10                  15
```

refer to p. 2.

same
refer to p. 2
please check all
of sequence #4
for "Xaa's".

VERIFICATION SUMMARY   DATE: 11/20/2000
PATENT APPLICATION: US/09/312,596   TIME: 08:38:39

Input Set : A:\593601.app
Output Set: N:\CRF3\11202000\I312596.raw

```
L:90 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:90 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:90 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:90 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:90 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:2
L:93 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:93 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:93 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:93 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
M:340 Repeated in SeqNo:2
L:108 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:108 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:108 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:108 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:117 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:117 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:117 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:117 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:120 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:120 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:120 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:120 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:123 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:123 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:123 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:123 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:252 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:252 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:252 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:252 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:261 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:261 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:261 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:261 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:270 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:270 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:270 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:270 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:285 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:2
L:285 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:2
L:285 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:2
L:285 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:326 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4
L:326 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:326 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:326 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4
L:326 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:4
L:389 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:4
```

VERIFICATION SUMMARY   DATE: 11/20/2000
PATENT APPLICATION: US/09/312,596   TIME: 08:38:39

Input Set : A:\593601.app
Output Set: N:\CRF3\11202000\I312596.raw

L:389 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4
L:389 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:4
L:389 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:4
M:340 Repeated in SeqNo 4
L:392 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:392 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:4